IN THE CLAIMS:

1. (Currently amended) A protein structure comprising a plurality of first peptide monomer units arranged in a first strand and a plurality of second peptide monomer units arranged in a second strand wherein the first and second monomer units comprise ~~the~~ a heptad repeat motif (gabcdef~~g~~ ;SEQ ID NO: 19) ~~and/or the hendecad repeat motif (abcdefghijk)~~, and wherein ~~a pair of asparagines, arginines, lysines or other complementary residues in the "a" position on at least one pair of corresponding first and second monomer units ensures that~~ the first strand and the second strand form a staggered parallel heterodimer coiled coil structure.

2. (Original) A protein structure according to claim 1, wherein a first peptide monomer unit inthe first strand extends beyond a corresponding second peptide monomer unit in the second strand in the direction of the strands.

3. (Currently amended) A protein structure according to any one of claims 1 ~~to 2~~ in which at least one charged amino acid residue of a first peptide monomer unit is arranged to attract an oppositely-charged amino acid residue of a second peptide monomer unit.

4. (Original) A protein structure according to claim 3 in which the charged amino acid residue is in an end portion of the first peptide monomer unit which extends beyond the corresponding second peptide monomer unit in the second strand.

5. (Currently amended) A protein structure according to ~~any one of the preceding claims~~ claim 1 in which at least one strand consists solely of first or second peptide monomer units respectively.

6. (Currently amended) ~~A protein structure according to any one of the preceding claims wherein one or more of the other "a" positions of the first and second monomer units is a hydrophobic residue.~~ A protein structure comprising a first peptide monomer unit arranged in a first strand and a second peptide monomer unit arranged in a second strand wherein the first and second monomer units comprise a heptad repeat motif (gabcdef), wherein the first peptide monomer unit comprises an amino acid sequence as shown in SEQ ID NO: 20 and the second

peptide monomer unit comprises an amino acid sequence as shown in SEQ ID NO: 21, and wherein the first strand and the second strand form a staggered parallel heterodimer coiled coil structure.

7. (Canceled) ~~A protein structure according to claim 6, wherein the hydrophobic residue is selected from isoleucine or valine.~~

8. (Canceled) ~~A protein structure according to anyone of the preceding claims having a leucine at one or more of the "d" positions of the first and second monomer units.~~

9. (Currently amended) A protein structure according to ~~any one of the preceding claims~~ claim 1 having oppositely-charged or otherwise complementary residues at positions "g" and "e" of respective monomer units.

10. (Canceled) ~~A protein structure according to claim 9 in which the opposite-charged residues are glutamic acid and lysine residues or arginine and aspartic acid residues or synthetic derivatives of these amino acid residues.~~

11. (Currently amended) A protein structure according to ~~any preceding~~ claim 1 in which the structure is stabilised by pairs of asparagine, arginine, lysine or other complementary residues provided by corresponding first and second peptide monomer units.

12. (Currently amended) A protein structure according to ~~any preceding~~ claim 1 which is arranged to form a tubular structure.

13. (Original) A protein structure according to claim 12 in which the repeat motifs are offset by two or more amino acid positions in sequence whereby the peptide monomer units form a cylinder.

14. (Currently amended) A protein structure according to ~~any preceding~~ claim 1 in which the first and second peptide monomer units have the sequence:

a) KIAALKQKIASLKQEIDALEYENDALEQ (SAF-pl; SEQ ID NO: 1) and

b) KIRALKAKNAHLKQEIAALEQEIAALEQ (SAF-p2; SEQ ID NO: 2) respectively; or

c) KIAALKQKIAALKQEIDALEYENDALEQ (SAF-plA; SEQ ID NO: 3) and

d) KIRALKWKNAHLKQEIAALEQEIAALEQ (SAF-p2C; SEQ ID NO: 4) respectively; or

e) KIAALKQKIASLKQEIDALEYENDALEQ (SAF-p1C; SEQ ID NO: 1) and

f) KIRALKWKNAHLKQEIAALEQEIAALEQ (SAF-p2C; SEQ ID NO: 4) respectively.

15. (Currently amended) A peptide monomer unit for use in preparing a protein structure the peptide monomer unit having an amino acid sequence selected from:

a) KIAALKQKIASLKQEIDALEYENDALEQ (SAF-pl; SEQ ID NO: 1);

b) KIRALKAKNAHLKQEIAALEQEIAALEQ (SAF-p2; SEQ ID NO: 2);

c) KIAALKQKIAALKQEIDALEYENDALEQ (SAF-p1A; SEQ ID NO: 3);

d) KIRALKWKNAHLKQEIAALEQEIAALEQ (SAF-p2C; SEQ ID NO: ~~5~~ 4); and

e) KIAALKQKIASLKQEIDALEYENDALEQ (SAF-p1C; SEQ ID NO: 1). ~~; and~~

~~d) KIRALKWKNAHLKQEIAALEQEIAALEQ (SAF-p2C; SEQ ID NO: 5).~~

16. (Currently amended) A protein structure according to any one of claims ~~1 to 14~~ 1-6, 9, 11-14 or a peptide monomer unit according to claim 15 wherein at least one amino acid residue is derivatised.

17. (Currently amended) A branching self-assembling fibre comprising two or more protein structures according to anyone of claims 1 to 6, 9, and 11, coupled together to form a T-shaped conjugated structure.

18. (Original) The branching self-assembling fibre of claim 17, wherein at least one of the protein structures comprises one or more central cysteine residues, and at least one other protein structure comprises a terminal cysteine residue.

19. (Currently amended) A method of producing protein structures, the method comprising providing a mixture of first and second monomer units which associate to form a protein structure according to any one of claims ~~1 to 14~~ 1-6, 9, 11-14, wherein the first and second monomer units comprise the heptad repeat motif (gabcdefg) ~~and/or the hendecad repeat motif (abcdefghijk)~~.

20. (Original) A method according to claim 19 in which the protein structure is derivatised.

21. (Currently amended) A method according to claim 19 ~~or 20~~ in which the protein structure is stabilised by cross-linking.

22. (Currently amended) A protein fibre produced by an association of protein structures according to any one of claims ~~1 to 14~~ 1-6, 9, 11-14.

23. (Currently amended) A kit for making a protein structure, the kit comprising first and second peptide monomer units which associate to form a protein structure according to any one of claims ~~1 to 14~~ 1-6, 9, 11-14 ~~or a protein fibre according to claim 22~~, wherein the first and second monomer units comprise the heptad repeat motif (gabcdefg) ~~and/or the hendecad repeat motif (abcdefghijk)~~.

24. (Currently amended) A two dimensional grid comprising a protein structure according to any one of claims ~~1 to 14~~ 1-6, 9, 11-14 ~~or a protein fibre according to claim 22~~.

25. (Currently amended) A three dimensional matrix comprising a protein structure according to any one of claims ~~1 to 14~~ 1-6, 9, 11-14 ~~or a protein fibre according to claim 22~~.

26. (Original) A matrix according to claim 25 which is managed to assemble in solution.

27. (Currently amended) A matrix according to claim 25 ~~or claim 26~~, wherein one or more binders is fused to the protein structure, wherein the one or more binders are aligned to give high avidities for one or more target entities.

28. (Currently amended) A matrix according to anyone of claims 25 ~~to 27~~ which is arranged to bind one or more target entities.

29. (Original) A matrix according to claim 28 which is arranged to bind viruses.

30. (Currently amended) A method of forming a matrix according to ~~any one of claims~~ claim 25 ~~to 29~~ in which a mixture of separate first and second monomer units is provided, wherein the first and second monomer units comprise the heptad repeat motif (gabcdef~~g~~ ;SEQ ID NO: 19) ~~and/or the hendecad repeat motif (abcdefghijk)~~ and are caused to associate to form a plurality of protein structures ~~according to any one of claims 1 to 14~~, wherein the protein structures assemble to form a three-dimensional matrix.

31. (Original) A method according to claim 30 in which the matrix is formed *in situ*.

32. (Currently amended) A method for controlling the production of a synthetic polymer~~s~~ comprising assembling a protein structure in accordance to any one of claims ~~1 to 14~~ 1-6, 9, 11-14 in association with the polymer.

33. (Original) A method according to claim 32 in which the protein structure is removed after synthesis of the polymer.

34. (Currently amended) A tip for use in Atomic Force Microscopy comprising a protein structure according to anyone of claims ~~1 to 14~~ 1-6, 9, 11-14.